



OIPE

## RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/10/051,902

TIME: 10:25:24

Input Set : N:\Crf3\RULE60\10051902.raw.txt

Output Set: N:\CRF3\02282002\J051902.raw

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1 <110> APPLICANT: Allen, Steve
2      Hitz, Bill
3      Kinney, Tony
4      Tingey, Scott
5 <120> TITLE OF INVENTION: Plant Sugar Transport Proteins
6 <130> FILE REFERENCE: BB-1163
7 <140> CURRENT APPLICATION NUMBER: 10/051,902
C--> 8 <141> CURRENT FILING DATE: 2002-01-17
9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/291,922
W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-14
11 <160> NUMBER OF SEQ ID NOS: 30
12 <170> SOFTWARE: Microsoft Office 97
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 2824
16 <212> TYPE: DNA
17 <213> ORGANISM: Zea mays
18 <220> FEATURE:
19 <221> NAME/KEY: unsure
20 <222> LOCATION: (29)
21 <220> FEATURE:
22 <221> NAME/KEY: unsure
23 <222> LOCATION: (622)
24 <220> FEATURE:
25 <221> NAME/KEY: unsure
26 <222> LOCATION: (636)
27 <220> FEATURE:
28 <221> NAME/KEY: unsure
29 <222> LOCATION: (638)
30 <220> FEATURE:
31 <221> NAME/KEY: unsure
32 <222> LOCATION: (669)
33 <220> FEATURE:
34 <221> NAME/KEY: unsure
35 <222> LOCATION: (771)
36 <220> FEATURE:
37 <221> NAME/KEY: unsure
38 <222> LOCATION: (822)
39 <220> FEATURE:
40 <221> NAME/KEY: unsure
41 <222> LOCATION: (856)
42 <220> FEATURE:
43 <221> NAME/KEY: unsure
44 <222> LOCATION: (889)

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```

45 (220) FEATURE:
46 (221) NAME/KEY: unsure
47 (222) LOCATION: (896)
48 (220) FEATURE:
49 (221) NAME/KEY: unsure
50 (222) LOCATION: (944)
51 (400) SEQUENCE: 1
W--> 52      cccaccccc  tccactccac  taccacggng  gcacggcctg  cctctgcagc  tctgccctgc  60
53      tccgcacccc  tcgctctcca  accccaacgc  gcggcgttgc  taaaattcac  ctcagcgcg  120
54      actccagttt  ggccacctca  ccacccgcgc  ccgctgttta  agaaggcccc  ggcgccgatc  180
55      ggggatcacg  aaccttgccc  gccgctgcgc  gagtgggggc  gtagatttcc  ggcggccatg  240
56      gggggcgccg  tgatggtcgc  catcgcgccc  tctatcgcca  acttgctgca  gggctgggac  300
57      aatgcgacaa  ttgctggagc  cgtcctgtac  ataaagaagg  aattcaacct  gcagagcgag  360
58      cctctgatcg  aaggcctcat  cgtcgccatg  ttcctcattg  gggcaacagt  catcacaaca  420
59      tctccggggc  caagggtcga  ctgcgttggt  aggaggccca  tgctggtcgc  ctgggctgtc  480
60      ctctacttgc  tcagtgggct  ggtgatgctt  tgggcgcca  ttgtgtacat  cttgctcttc  540
61      gcaaggctca  ttgatgggtt  cggtatcggt  ttggcggtca  cacttgttcc  tctctacatc  600
W--> 62      tccgaaactg  caccgcacag  anattcttgg  ggctgntnga  acacgttgcc  gcagttcatt  660
W--> 63      ggggtcagng  gagggatggt  cctctcctac  tgcattggtg  ttgggatgtc  cctcatgccc  720
W--> 64      aaacctgatt  ggaggtcat  gcttgaggat  ctgtcgatcc  cgtcacttat  ntactttgga  780
W--> 65      ctgactgtct  tctacttgcc  tgaatcacca  aggtggcttg  tnagcaaagg  aaggatggcg  840
W--> 66      gaggcgaaga  gagtntgca  aaggctgcgc  ggaagagaag  atgtctcang  ggaganggct  900
W--> 67      cttctagtgt  aaggtttggg  ggtcggtaaa  gatacacgta  ttttnagagta  catcattgga  960
68      cctgccaccg  aggcagccga  tgatcttgta  actgacggtg  ataaggaaca  aatcacactt  1020
69      tatgggcctg  aagaaggcca  gtcattggat  gctcgacctt  ctaagggacc  catcatgctt  1080
70      ggaagtgtgc  tttctcttgc  atctcgatca  gggagcatgg  tgaaccagag  tgtacctctt  1140
71      atggatccga  ttgtgacact  ttttggtagt  gtccatgaga  atatgcctca  agctggagga  1200
72      agtatgagga  gcacattggt  tccaaacttt  ggaagtatgt  tcagtgtcac  agatcagcat  1260
73      gccaaaaatg  agcagtggga  tgaagagaat  cttcataggg  atgacgagga  gtacgcattc  1320
74      gatggtgcag  gaggtgacta  tgaggacaat  ctccatagcc  cattgctgtc  caggcaggca  1380
75      acaggtgcgc  aagggaagga  cattgtgcac  catggtcacc  gtggaagtgc  tttgagcatg  1440
76      agaaggcaaa  gcctcttagg  ggaggggtga  gatggtgtga  gcagcactga  tatcggtggg  1500
77      ggatggcagc  ttgcttgga  atggtcagag  aagggaaggt  agaattggtg  aaaggaaggt  1560
78      ggtttcaaaa  gagtctactt  gcaccaagag  ggagttcctg  gctcaagaag  gggctcaatt  1620
79      gtttcaactt  ccggtggtgg  cgatgttctt  gagggtagtg  agtttgtaca  tgctgctgct  1680
80      ttagtaagtc  agtcagcact  tttctcaaag  ggtcttgctg  aaccacgcac  gtcagatgct  1740
81      gccatggttc  acccatctga  ggtagctgcc  aaaggttcac  gttggaaaga  tttgtttgaa  1800
82      cctggagtga  ggcgtgccct  gttagtcggt  gttggaattc  agatccttca  acagtttgct  1860
83      ggaataaacg  gtgttctgta  ctatacccca  caaattcttg  agcaagctgg  tgtggcagtt  1920
84      attctttcca  aatttggtct  cagctcgcca  tcagcatcca  tcttgatcag  ttctctcact  1980
85      acctactaa  tgcttccttg  cattggcttt  gccatgctgc  ttatggatct  ttccggaaga  2040
86      aggtttttgc  tgctaggcac  aattccaatc  ttgatagcat  ctctagttat  cctggttgtg  2100
87      tccaatctaa  ttgatttggg  tacactagcc  catgctttgc  tctccaccat  cagtgttata  2160
88      gtctacttct  gctgcttcgt  tatgggattt  ggtcccatcc  ccaacatttt  atgtgcagag  2220
89      atctttccaa  ccagggttcg  tggcctctgt  attgccattt  gtgcctttac  attctggatc  2280
90      ggagatatca  tcgtcaccta  cagccttcct  gtgatgctga  atgctattgg  actggcgggt  2340
91      gttttcagca  tatatgcagt  cgtatgcttg  atttcccttg  tgttcgtctt  ccttaaggtc  2400
92      cctgagacaa  aggggatgcc  ccttgagggt  attaccgaat  tctttgcagt  tgggtgcgaag  2460
93      caagcggtcg  caaaagccta  atttcttttg  tacctttgtg  tgcaactatt  gcactgtaag  2520

```

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```

94      tttagaaaatt gaagggggttt caccaagaag ctgaggagaat tacttttggat ttgtgttaa 2580
95      gtttaagggaa cgaacatctg ctcatgctcc tcaaacggta aaaaagagtc cctcaatggc 2640
96      aaataggagt cgttaagttg tcaatgtcat ttaccatattg ttttacctat ttgtactgta 2700
97      ttataagtca agctattcaa cgctgggttg tgctagaaat ctttagaaca aagatgataa 2760
98      tgatctgata tgatgttata atattcaaat ctcaaataaa gaaaatatcg tttctcaaaa 2820
99      aaaa 2824

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101 &lt;210&gt; SEQ ID NO: 2

102 &lt;211&gt; LENGTH: 747

103 &lt;212&gt; TYPE: PRI

104 &lt;213&gt; ORGANISM: Zea mays

105 &lt;220&gt; FEATURE:

106 &lt;221&gt; NAME/KEY: UNSURE

107 &lt;222&gt; LOCATION: (129)

108 &lt;220&gt; FEATURE:

109 &lt;221&gt; NAME/KEY: UNSURE

110 &lt;222&gt; LOCATION: (133)..(134)

111 &lt;220&gt; FEATURE:

112 &lt;221&gt; NAME/KEY: UNSURE

113 &lt;222&gt; LOCATION: (144)

114 &lt;220&gt; FEATURE:

115 &lt;221&gt; NAME/KEY: UNSURE

116 &lt;222&gt; LOCATION: (178)

117 &lt;220&gt; FEATURE:

118 &lt;221&gt; NAME/KEY: UNSURE

119 &lt;222&gt; LOCATION: (207)

120 &lt;220&gt; FEATURE:

121 &lt;221&gt; NAME/KEY: UNSURE

122 &lt;222&gt; LOCATION: (218)

123 &lt;220&gt; FEATURE:

124 &lt;221&gt; NAME/KEY: UNSURE

125 &lt;222&gt; LOCATION: (220)

126 &lt;220&gt; FEATURE:

127 &lt;221&gt; NAME/KEY: UNSURE

128 &lt;222&gt; LOCATION: (236)

129 &lt;400&gt; SEQUENCE: 2

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130      Met Gly Gly Ala Val Met Val Ala Ile Ala Ala Ser Ile Gly Asn Leu
131      1          5          10          15
132      Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
133      20          25          30
134      Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
135      35          40          45
136      Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Thr Ser Pro Gly
137      50          55          60
138      Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala
139      65          70          75          80
140      Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val
141      85          90          95
142      Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu
143      100          105          110

```

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144	Ala	Val	Thr	Leu	Val	Pro	Leu	Tyr	Ile	Ser	Glu	Thr	Ala	Pro	His	Arg
145			115					120					125			
W--> 146	Xaa	Ser	Trp	Gly	Xaa	Xaa	Asn	Thr	Leu	Pro	Gln	Phe	Ile	Gly	Val	Xaa
147			130				135					140				
148	Gly	Gly	Met	Phe	Leu	Ser	Tyr	Cys	Met	Val	Phe	Gly	Met	Ser	Leu	Met
149	145					150					155					160
150	Pro	Lys	Pro	Asp	Trp	Arg	Leu	Met	Leu	Gly	Val	Leu	Ser	Ile	Pro	Ser
151					165					170					175	
W--> 152	Leu	Xaa	Tyr	Phe	Gly	Leu	Thr	Val	Phe	Tyr	Leu	Pro	Glu	Ser	Pro	Arg
153				180					185					190		
W--> 154	Trp	Leu	Val	Ser	Lys	Gly	Arg	Met	Ala	Glu	Ala	Lys	Arg	Val	Xaa	Gln
155			195					200					205			
W--> 156	Arg	Leu	Arg	Gly	Arg	Glu	Asp	Val	Ser	Xaa	Glu	Xaa	Ala	Leu	Leu	Val
157		210					215					220				
W--> 158	Glu	Gly	Leu	Gly	Val	Gly	Lys	Asp	Thr	Arg	Ile	Xaa	Glu	Tyr	Ile	Ile
159	225					230					235					240
160	Gly	Pro	Ala	Thr	Glu	Ala	Ala	Asp	Asp	Leu	Val	Thr	Asp	Gly	Asp	Lys
161				245							250				255	
162	Glu	Gln	Ile	Thr	Leu	Tyr	Gly	Pro	Glu	Glu	Gly	Gln	Ser	Trp	Ile	Ala
163				260						265				270		
164	Arg	Pro	Ser	Lys	Gly	Pro	Ile	Met	Leu	Gly	Ser	Val	Leu	Ser	Leu	Ala
165			275					280					285			
166	Ser	Arg	His	Gly	Ser	Met	Val	Asn	Gln	Ser	Val	Pro	Leu	Met	Asp	Pro
167		290					295					300				
168	Ile	Val	Thr	Leu	Phe	Gly	Ser	Val	His	Glu	Asn	Met	Pro	Gln	Ala	Gly
169	305					310					315					320
170	Gly	Ser	Met	Arg	Ser	Thr	Leu	Phe	Pro	Asn	Phe	Gly	Ser	Met	Phe	Ser
171				325						330					335	
172	Val	Thr	Asp	Gln	His	Ala	Lys	Asn	Glu	Gln	Trp	Asp	Glu	Glu	Asn	Leu
173				340					345					350		
174	His	Arg	Asp	Asp	Glu	Glu	Tyr	Ala	Ser	Asp	Gly	Ala	Gly	Gly	Asp	Tyr
175			355					360					365			
176	Glu	Asp	Asn	Leu	His	Ser	Pro	Leu	Leu	Ser	Arg	Gln	Ala	Thr	Gly	Ala
177		370					375					380				
178	Glu	Gly	Lys	Asp	Ile	Val	His	His	Gly	His	Arg	Gly	Ser	Ala	Leu	Ser
179	385					390					395					400
180	Met	Arg	Arg	Gln	Ser	Leu	Leu	Gly	Glu	Gly	Gly	Asp	Gly	Val	Ser	Ser
181				405						410					415	
182	Thr	Asp	Ile	Gly	Gly	Gly	Trp	Gln	Leu	Ala	Trp	Lys	Trp	Ser	Glu	Lys
183				420					425					430		
184	Glu	Gly	Glu	Asn	Gly	Arg	Lys	Glu	Gly	Gly	Phe	Lys	Arg	Val	Tyr	Leu
185			435					440					445			
186	His	Gln	Glu	Gly	Val	Pro	Gly	Ser	Arg	Arg	Gly	Ser	Ile	Val	Ser	Leu
187		450					455					460				
188	Pro	Gly	Gly	Gly	Asp	Val	Leu	Glu	Gly	Ser	Glu	Phe	Val	His	Ala	Ala
189	465					470					475					480
190	Ala	Leu	Val	Ser	Gln	Ser	Ala	Leu	Phe	Ser	Lys	Gly	Leu	Ala	Glu	Pro
191				485						490					495	
192	Arg	Met	Ser	Asp	Ala	Ala	Met	Val	His	Pro	Ser	Glu	Val	Ala	Ala	Lys

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```

193          500          505          510
194    Gly Ser Arg Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu
195          515          520          525
196    Leu Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe Ala Gly Ile Asn
197          530          535          540
198    Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala
199    545          550          555          560
200    Val Ile Leu Ser Lys Phe Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu
201          565          570          575
202    Ile Ser Ser Leu Thr Thr Leu Leu Met Leu Pro Cys Ile Gly Phe Ala
203          580          585          590
204    Met Leu Leu Met Asp Leu Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr
205          595          600          605
206    Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu Val Val Ser Asn Leu
207          610          615          620
208    Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu Ser Thr Ile Ser Val
209    625          630          635          640
210    Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn
211          645          650          655
212    Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Leu Cys Ile
213          660          665          670
214    Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp Ile Ile Val Thr Tyr
215          675          680          685
216    Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Ser
217          690          695          700
218    Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val Phe Val Phe Leu Lys
219    705          710          715          720
220    Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe
221          725          730          735
222    Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala
223          740          745
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 443
227 <212> TYPE: DNA
228 <213> ORGANISM: Oryza sativa
229 <220> FEATURE:
230 <221> NAME/KEY: unsure
231 <222> LOCATION: (193)
232 <220> FEATURE:
233 <221> NAME/KEY: unsure
234 <222> LOCATION: (388)
235 <220> FEATURE:
236 <221> NAME/KEY: unsure
237 <222> LOCATION: (435)
238 <220> FEATURE:
239 <221> NAME/KEY: unsure
240 <222> LOCATION: (439)
241 <400> SEQUENCE: 3
242    gaagagctca cccccccccc ctcggccctg gactccctcc tccaaatctc ccctaaaagc 60

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Input Set : N:\Crf3\RULE60\10051902.raw.txt

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L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:10 M:256 W: Invalid Numeric Header Field. Wrong Prior FILING DATE:YYYY-MM-DD  
L:52 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:62 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:63 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:64 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:65 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:66 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:67 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:146 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:152 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:154 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:156 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:158 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:245 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:248 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:249 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:270 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:278 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:611 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:612 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:807 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:809 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:810 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:812 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17



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Input Set : N:\Crif3\RULE60\10051902.raw.txt

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L:814 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:814 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:815 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17  
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:847 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:849 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:855 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:1029 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22  
L:1029 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22